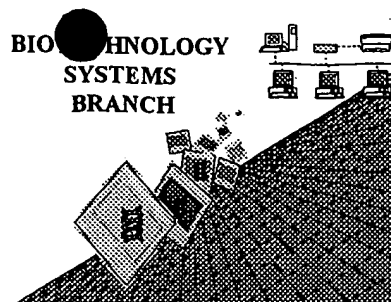# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/701,395_

Source: _PCT 09,_

Date Processed by STIC: _1/23/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

```
                  RAW SEQUENCE LISTING              DATE: 01/23/2001
                  PATENT APPLICATION:  US/09/701,395    TIME: 11:13:18

                    Input Set  : A:\108172-00022.txt
                    Output Set: N:\CRF3\01232001\I701395.raw
```

see p. 6

Does Not Comply
Corrected Diskette Needed

```
     4 <110> APPLICANT: CUNNINGHAM JR., FRANCIS X.
     5           SUN, ZAIREN
     7 <120> TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
     8           METHODS OF USE THEREOF
    10 <130> FILE REFERENCE: 8172-9023
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/701,395
C--> 13 <141> CURRENT FILING DATE: 2000-12-04
    15 <150> PRIOR APPLICATION NUMBER: 09/088,724
    16 <151> PRIOR FILING DATE: 1998-06-02
    18 <150> PRIOR APPLICATION NUMBER: 09/088,725
    19 <151> PRIOR FILING DATE: 1998-06-02
    21 <160> NUMBER OF SEQ ID NOS: 61
    23 <170> SOFTWARE: PatentIn Ver. 2.0
    25 <210> SEQ ID NO: 1
    26 <211> LENGTH: 1860
    27 <212> TYPE: DNA
    28 <213> ORGANISM: Arabidopsis thaliana
    30 <220> FEATURE:
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    32 <222> LOCATION: (109)..(1680)
    34 <400> SEQUENCE: 1
C--> 35 acaaaaggaa ataattagat tcctctttct gcttgctata ccttgataga acaatataac        60
    37 aatggtgtaa gtcttctcgc tgtattcgaa attatttgga ggaggaaa atg gag tgt       117
    38                                                          Met Glu Cys
    39                                                            1
    41 gtt ggg gct agg aat ttc gca gca atg gcg gtt tca aca ttt ccg tca       165
    42 Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser
    43           5                   10                  15
    45 tgg agt tgt cga agg aaa ttt cca gtg gtt aag aga tac agc tat agg       213
    46 Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr Ser Tyr Arg
    47  20                  25                  30                  35
    49 aat att cgt ttc ggt ttg tgt agt gtc aga gct agc ggc ggc gga agt       261
    50 Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly Gly Gly Ser
    51           40                  45                  50
    53 tcc ggt agt gag agt tgt gta gcg gtg aga gaa gat ttc gct gac gaa       309
    54 Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe Ala Asp Glu
    55           55                  60                  65
    57 gaa gat ttt gtg aaa gct ggt ggt tct gag att cta ttt gtt caa atg       357
    58 Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe Val Gln Met
    59           70                  75                  80
    61 cag cag aac aaa gat atg gat gaa cag tct aag ctt gtt gat aag ttg       405
    63 Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val Asp Lys Leu
    64  85                  90                  95
    66 cct cct ata tca att ggt gat ggt gct ttg gat cat gtg gtt att ggt       453
    67 Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val Val Ile Gly
    68 100                 105                 110                 115
    70 tgt ggt cct gct ggt tta gcc ttg gct gca gaa tca gct aag ctt gga       501
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/701,395

DATE: 01/23/2001
TIME: 11:13:18

Input Set : A:\108172-00022.txt
Output Set: N:\CRF3\01232001\I701395.raw

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71 Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly
72               120                   125                   130
74 tta aaa gtt gga ctc att ggt cca gat ctt cct ttt act aac aat tac     549
75 Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr
76               135                   140                   145
78 ggt gtt tgg gaa gat gaa ttc aat gat ctt ggg ctg caa aaa tgt att     597
79 Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln Lys Cys Ile
80               150                   155                   160
82 gag cat gtt tgg aga gag act att gtg tat ctg gat gat gac aag cct     645
83 Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp Asp Lys Pro
84               165                   170                   175
86 att acc att ggc cgt gct tat gga aga gtt agt cga cgt ttg ctc cat     693
87 Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg Leu Leu His
88 180                   185                   190                   195
90 gag gag ctt ttg agg agg tgt gtc gag tca ggt gtc tcg tac ctt agc     741
91 Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser
92               200                   205                   210
94 tcg aaa gtt gac agc ata aca gaa gct tct gat ggc ctt aga ctt gtt     789
95 Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu Arg Leu Val
96               215                   220                   225
98 gct tgt gac gac aat aac gtc att ccc tgc agg ctt gcc act gtt gct     837
99 Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala Thr Val Ala
100               230                   235                   240
102 tct gga gca gct tcg gga aag ctc ttg caa tac gaa gtt ggt gga cct    885
103 Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly Pro
104               245                   250                   255
106 aga gtc tgt gtg caa act gca tac ggc gtg gag gtt gag gtg gaa aat    933
107 Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn
108 260                   265                   270                   275
110 agt cca tat gat cca gat caa atg gtt ttc atg gat tac aga gat tat    981
111 Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr Arg Asp Tyr
112               280                   285                   290
114 act aac gag aaa gtt cgg agc tta gaa gct gag tat cca acg ttt ctg    1029
115 Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro Thr Phe Leu
116               295                   300                   305
118 tac gcc atg cct atg aca aag tca aga ctc ttc ttc gag gag aca tgt    1077
119 Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu Glu Thr Cys
120               310                   315                   320
122 ttg gcc tca aaa gat gtc atg ccc ttt gat ttg cta aaa acg aag ctc    1125
123 Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys Thr Lys Leu
125               325                   330                   335
127 atg tta aga tta gat aca ctc gga att cga att cta aag act tac gaa    1173
128 Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys Thr Tyr Glu
129 340                   345                   350                   355
131 gag gag tgg tcc tat atc cca gtt ggt ggt tcc ttg cca aac acc gaa    1221
132 Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
133               360                   365                   370
135 caa aag aat ctc gcc ttt ggt gct gcc gct agc atg gta cat ccc gca    1269
136 Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
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RAW SEQUENCE LISTING   DATE: 01/23/2001
PATENT APPLICATION: US/09/701,395   TIME: 11:13:18

Input Set : A:\108172-00022.txt
Output Set: N:\CRF3\01232001\I701395.raw

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137               375                 380                 385
139 aca ggc tat tca gtt gtg aga tct ttg tct gaa gct cca aaa tat gca        1317
140 Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala
141           390                 395                 400
143 tca gtc atc gca gag ata cta aga gaa gag act acc aaa cag atc aac        1365
144 Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys Gln Ile Asn
145     405                 410                 415
147 agt aat att tca aga caa gct tgg gat act tta tgg cca cca gaa agg        1413
148 Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg
149 420                 425                 430                 435
151 aaa aga cag aga gca ttc ttt ctc ttt ggt ctt gca ctc ata gtt caa        1461
152 Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln
153               440                 445                 450
155 ttc gat acc gaa ggc att aga agc ttc ttc cgt act ttc ttc cgc ctt        1509
156 Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe Phe Arg Leu
157           455                 460                 465
159 cca aaa tgg atg tgg caa ggg ttt cta gga tca aca tta aca tca gga        1557
160 Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu Thr Ser Gly
161           470                 475                 480
163 gat ctc gtt ctc ttt gct tta tac atg ttc gtc att tca cca aac aat        1605
164 Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser Pro Asn Asn
165     485                 490                 495
167 ttg aga aaa ggt ctc atc aat cat ctc atc tct gat cca acc gga gca        1653
168 Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro Thr Gly Ala
169 500                 505                 510                 515
171 acc atg ata aaa acc tat ctc aaa gta tgatttactt atcaactctt            1700
172 Thr Met Ile Lys Thr Tyr Leu Lys Val
173               520
175 aggtttgtgt atatatatgt tgatttatct gaataatcga tcaaagaatg gtatgtgggt      1760
177 tactaggaag ttggaaacaa acatgtatag aatctaagga gtgatcgaaa tggagatgga      1820
179 aacgaaaaga aaaaatcag tcttttgtttt gtggttagtg                            1860
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 524
184 <212> TYPE: PRT
185 <213> ORGANISM: Arabidopsis thaliana
187 <400> SEQUENCE: 2
188 Met Glu Cys Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr
189 1               5                 10                  15
191 Phe Pro Ser Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr
192               20                  25                  30
194 Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
195       35                  40                  45
197 Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
198       50                  55                  60
200 Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
201 65                  70                  75                  80
203 Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
204               85                  90                  95
206 Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
```

```
207            100              105              110
209 Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
210          115              120              125
212 Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
213     130              135              140
215 Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
216 145              150              155              160
218 Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
219              165              170              175
221 Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
222          180              185              190
224 Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
225          195              200              205
227 Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
228     210              215              220
230 Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
231 225              230              235              240
233 Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
234          245              250              255
236 Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
237          260              265              270
239 Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr
240     275              280              285
242 Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
243     290              295              300
245 Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
246 305              310              315              320
249 Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys
250          325              330              335
252 Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys
253          340              345              350
255 Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro
256     355              360              365
258 Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
259     370              375              380
261 His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
262 385              390              395              400
264 Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
265          405              410              415
267 Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
268          420              425              430
270 Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
271     435              440              445
273 Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
274     450              455              460
276 Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
277 465              470              475              480
279 Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
280          485              490              495
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RAW SEQUENCE LISTING   DATE: 01/23/2001
PATENT APPLICATION: US/09/701,395   TIME: 11:13:18

Input Set : A:\108172-00022.txt
Output Set: N:\CRF3\01232001\1701395.raw

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282 Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
283           500               505               510
285 Thr Gly Ala Thr Met Ile Lys Thr Tyr Leu Lys Val
286           515               520
288 <210> SEQ ID NO: 3
289 <211> LENGTH: 956
290 <212> TYPE: DNA
291 <213> ORGANISM: Arabidopsis thaliana
293 <400> SEQUENCE: 3
C--> 294 gctctttctc ctcctcctct accgattccc gactccgcct cccgaaatcc ttatccggat      60
296 tctctccgtc tcttcgattt aaacgctttt ctgtctgtta cgtcgtcgaa gaacggagac     120
298 agaattctcc gattgagaac gatgagagac cggagagcac gagctccaca aacgctatag     180
300 acgctgagta tctggcgttg cgtttggcgg agaaattgga gaggaagaaa tcggagaggt     240
302 ccacttatct aatcgctgct atgttgtcga gctttggtat cacttctatg gctgttatgg     300
304 ctgtttacta cagattctct tggcaaatgg agggaggtga gatctcaatg ttggaaatgt     360
306 ttggtacatt tgctctctct gttggtgctg ctgttggtat ggaattctgg gcaagatggg     420
308 ctcatagagc tctgtgtgca gcttctctat ggaatatgca tgagtcacat cacaaaccaa     480
311 gagaaggacc gtttgagcta aacgatgttt ttgctatagt gaacgctggt ccagcgattg     540
313 gtctcctctc ttatggattc ttcaataaag gactcgttcc tggtctctgc tttggcgccg     600
315 ggttaggcat aacggtgttt ggaatcgcct acatgtttgt ccacgatggt ctcgtgcaca     660
317 agcgtttccc tgtaggtccc atcgccgacg tcccttacct ccgaaaggtc gccgccgctc     720
319 accagctaca tcacacagac aagttcaatg gtgtaccata tggactgttt cttggaccca     780
321 aggaattgga agaagttgga ggaaatgaag agttagaraa ggagattagt cggagaatca     840
323 aatcatacaa aaaggcctcg ggctccgggt cgagttcgag ttcttgactt taaacaagtt     900
325 ttaaatccca aattctttttt ttgtcttctg tcattatgat catcttaaga cggtct         956
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 294
329 <212> TYPE: PRT
330 <213> ORGANISM: Arabidopsis thaliana
332 <400> SEQUENCE: 4
333 Ser Phe Ser Ser Ser Ser Thr Asp Phe Arg Leu Arg Leu Pro Lys Ser
334 1                5                10                15
336 Leu Ser Gly Phe Ser Pro Ser Leu Arg Phe Lys Arg Phe Ser Val Cys
337              20                25                30
339 Tyr Val Val Glu Glu Arg Arg Gln Asn Ser Pro Ile Glu Asn Asp Glu
340           35                40                45
342 Arg Pro Glu Ser Thr Ser Ser Thr Asn Ala Ile Asp Ala Glu Tyr Leu
343        50                55                60
345 Ala Leu Arg Leu Ala Glu Lys Leu Glu Arg Lys Lys Ser Glu Arg Ser
346 65                70                75                80
348 Thr Tyr Leu Ile Ala Ala Met Leu Ser Ser Phe Gly Ile Thr Ser Met
349              85                90                95
351 Ala Val Met Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly
352           100               105               110
354 Glu Ile Ser Met Leu Glu Met Phe Gly Thr Phe Ala Leu Ser Val Gly
355           115               120               125
357 Ala Ala Val Gly Met Glu Phe Trp Ala Arg Trp Ala His Arg Ala Leu
358        130               135               140
360 Trp His Ala Ser Leu Trp Met Asn His Glu Ser His His Lys Pro Arg
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<210> 13
<211> 960
<212> DNA
<213> Tagetes erecta

Use lower-case letters for bases, when using new Sequence Rules format. Please correct globally.

<400> 13

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CCAAAAACAA CTCAAATCTC CTCCGTCGCT CTTACTCCGC CATGGGTGAC GACTCCGGCA    60

TGGATGCTGT TCAGCGACGT CTCATGTTTG ACGATGAATG CATTTTGGTG GATGAGTGTG   120

ACAATGTGGT GGGACATGAT ACCAAATACA ATTGTCACTT GATGGAGAAG ATTGAAACAG   180

GTAAAATGCT GCACAGAGCA TTCAGCGTTT TTCTATTCAA TTCAAAATAC GAGTTACTTC   240

TTCAGCAACG GTCTGCAACC AAGGTGACAT TTCCTTTAGT ATGGACCAAC ACCTGTTGCA   300

GCCATCCACT CTACAGAGAA TCCGAGCTTG TTCCCGAAAC GCCTGAGAGA ATGCTGCACA   360

GAGGANNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   420

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   480

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   540

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   600

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   660

NNNNNNNNNN NNNNNNNNNN TCATGTGCAA AAGGGTACAC TCACTGAATG CAATTTGATA   720

TGAAAACCAT ACACAAGCTG ATATAGAAAC ACACCCTCAA CCGAAAAGCA AGCCTAATAA   780

TTCGGGTTGG GTCGGGTCTA CCATCAATTG TTTTTTTCTT TTAACAACTT TTAATCTCTA   840

TTTGAGCATG TTGATTCTTG TCTTTTGTGT GTAAGATTTT GGGTTTCGTT TCAGTTGTAA   900

TAATGAACCA TTGATGGTTT GCAATTTCAA GTTCCTATCG ACATGTAGTG ATCTAAAAAA   960
```

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

also see item 10 on Erar Summary Sheet

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:294 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=3
L:554 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=9
L:594 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:636 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=11
L:684 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=12
L:729 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=13
L:741 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:741 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:741 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:741 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:741 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:745 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:745 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:745 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:745 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:747 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:747 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:747 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:747 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:749 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:749 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:749 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:749 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:751 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:751 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:751 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:751 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:1341 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=22
L:1521 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=24
L:1634 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:1634 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25

Input Set : A:\108172-00022.txt
Output Set: N:\CRF3\01232001\I701395.raw

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L:1634 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1634 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1634 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1743 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1743 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1840 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=28
L:1881 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=29
L:1931 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=30
L:1975 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=31
L:2015 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=32
L:2055 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=33
L:2125 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=34
L:2163 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=35
L:2782 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=46
L:3019 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48
L:3019 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:3019 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:3019 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:48
L:3019 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:48
```